SOE 20: Networks: From Topology to Dynamics V (with BP, DY)

Time: Thursday 16:00–17:15   Location: H44

SOE 20.1   Thu 16:00   H44

Eat the specialist: Some results on the stability of 100 billion food webs — •THILO GROSS — Max-Planck Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden

Ecological food webs are complex networks of feeding interactions, describing who-eats-who in an ecosystem. Previous theoretical results suggest that the dynamical stability of these webs should decrease with increasing number of species and network connections. Yet, large and densely-linked webs found in nature are highly stable. Identification of the properties promoting stability is therefore an important goal of ecological research. The approach of generalized modeling enables us to investigate the local stability of steady states in these webs with a higher degree of generality and efficiency than previous simulative approaches. Because of the complexity of the problem, a general food web model contains several thousand unknown parameters. However, the numerical efficiency of the generalized models is such that tens of billions of different realizations of plausible webs can be analyzed in reasonable computational time. This provides a sound basis for the statistical exploration of the high-dimensional parameter space. In this talk I will demonstrate the application of generalized modeling, in simple examples and in large food webs. The latter reveals certain topological properties having a strong impact on network stability.

SOE 20.2   Thu 16:15   H44

Regular graph properties of the plasmodial vein network of the slime mould *Physarum polycephalum* — WERNER BAUMGARTEN and •MARCUS HAUSER — Otto-von-Guericke-Universität Magdeburg, Abteilung Biophysik, Institut für Experimentelle Physik, Universitätsplatz 2, 39106 Magdeburg, Germany

The plasmodium of the slime mould *Physarum polycephalum* is a single multi-nucleate giant amoeboid cell. It forms a characteristic two-dimensional vein network, where the apical end of the plasmodium extends to search for new food sources, while the dense network of tubular veins is in charge of transport of protoplasm throughout the giant cell.

A graph theoretical analysis of the vein network of the *Physarum polycephalum* strain HU195×HU200 reveals that the nodes have exclusively the degree 3, i.e., each node connects to exactly three veins. This means that the vein network of this slime mould forms a regular cubic graph, and hence does not show small-world properties. The intensities of the edges (the vein segments) connecting a pair of nodes differ, thus forming a weighted graph. The distributions of the lengths and areas of the veins follow exponential distributions, while their widths are distributed either log-normally or normally. Interestingly, these functional dependencies are robust during the entire evolution of the growing plasmodial vein network of *Physarum polycephalum*.

SOE 20.3   Thu 16:30   H44

Feedback-mediated control of a spiral wave in a bidomain model of cardiac tissue — •EKATERINA ZHUCHKOVA, VLADIMIR ZYKOV, and HARALD ENGEL — Institut für Theoretische Physik, Technische Universität zu Berlin, Berlin, Germany

At the moment anti-tachycardia pacing (ATP) is the only low-energy therapy for ventricular tachyarrhythmias and it would be desirable since it prevents adverse side effects. However, ATP is not robust since its success/failure depends on many factors [1]. Using realistic

bidomain model for simulation of electrical activity in cardiac tissue together with a simplified Fenton-Karma ionic model for a cell, we show that spiral waves in the heart could be eliminated by repetitive extracellular stimulation. A spiral wave core can be guided towards boundaries by feedback forcing along a one-dimensional registering electrode [2]. Every time the spiral wave front is tangent to the registering electrode, an extracellular current is applied through stimulating electrodes. The amplitude of the stimulation is much less than the single-shock defibrillation threshold, which gives a possibility to use the proposed method as an alternative low-voltage defibrillation strategy.

[1] E. Zhuchkova and H. Engel, Robustness of local forcing in inhibition of reentry, IPACS Open Access Library (2009), accepted.

[2] J. Schlesner, V. S. Zykov, H. Brandtstädter, I. Gerdes and H. Engel, Efficient control of spiral wave location in an excitable medium with localized heterogeneities, NJP 10, 015003 (2008).

SOE 20.4   Thu 16:45   H44

Linking Molecular Simulations and Systemic Modelling — •TIHAMER GEYER and VOLKHARD HELMS — Zentrum für Bioinformatik, Universität des Saarlandes, D-66123 Saarbrücken

When modeling biological systems there is a gap of scales between the systemic models that try to describe the metabolism of a complete cell and the molecular biological descriptions focussing on the detailed processes of a single enzyme. We therefore proposed an agent based approch that allows to bridge between the two regimes.

For this, we set up the individual enzymes from their microscopic elementary reactions like the binding of a metabolite molecule to a binding site or the transfer of an electron from one site inside the protein to another. The respective numbers of these protein "building blocks" are then connected to metabolite pools via standardized connectors to set up the metabolic system under consideration. This pools-and-proteins model can thus be used to "convert" detailed molecular biological knowledge into a systems biological model for analyzis of the complete system.

To develop and test our approach we used the bacterial photosynthetic apparatus. But even for the "boringly" well-known system, many of the detailed kinetic constants were unknown. By comparing the behavior of the complete system to time-dependent experiments, we could determine the values and sensitivities of all parameters of our model. The thus parametrized protein modules allowed for new insights into their inner working and can be re-used to set up other, related systems.

SOE 20.5   Thu 17:00   H44

About scaling in the growth of clubs and communities — LU XIN[1], DIEGO RYBSKI[2], and •FREDRIK LILJEROS[1] — [1]Department of Sociology, Stockholm University, S-106 91 Stockholm, Sweden — [2]Potsdam Institute for Climate Impact Research, P.O. Box 60 12 03, 14412 Potsdam, Germany

Many systems comprise emergent power-laws in the growth rates with respect to the size of the units such as companies or cities. Here we study online communities and investigate the growth properties of clubs and social communities. We find power-law relations for the average growth rate and for the standard deviation. The quality of the data permits to analyze the growth – complementary to (temporal) correlations – on the basis of individuals behaving in a social context.